

SEQUENCE LISTING

<110> Novak, Julia E.
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 Dillon, Stacey R.
 Hammond, Angela K.

<120> NOVEL CYTOKINE ZALPHA11 LIGAND

<130> 99-16

<150> US 60/123,547

<151> 1999-03-09

<150> US 60/123,904

<151> 1999-03-11

<150> US 60/142,013

<151> 1999-07-01

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 Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met Val Ile Phe
 5 10 15

ttg ggg aca ctg gtc cac aaa tca agc tcc caa ggt caa gat cgc cac 151
 Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln Asp Arg His
 20 25 30 35

atg att aga atg cgt caa ctt ata gat att gtt gat cag ctg aaa aat 199
 Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys Asn
 40 45 50

tat gtg aat gac ttg gtc cct gaa ttt ctg cca gct cca gaa gat gta 247
 Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp Val
 55 60 65

gag aca aac tgt gag tgg tca gct ttt tcc tgt ttt cag aag gcc caa 295
 Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala Gln
 70 75 80

cta aag tca gca aat aca gga aac aat gaa agg ata atc aat gta tca 343
 Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val Ser
 85 90 95

att aaa aag ctg aag agg aaa cca cct tcc aca aat gca ggg aga aga 391
 Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg Arg
 100 105 110 115

cag aaa cac aga cta aca tgc cct tca tgt gat tct tat gag aaa aaa 439
 Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys
 120 125 130

cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc caa aag atg 487
 Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys Met
 135 140 145

att cat cag cat ctg tcc tct aga aca cac gga agt gaa gat tcc 532
 Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser
 150 155 160

tgaggatcta acttgcagtt ggacactatg ttacatactc taatatagta gtgaaagtca 592
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Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	Phe	Leu	Pro	Ala	Pro
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Asp	Ser														

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ytnccngcnc	cngargaygt	ngaracnaay	tgygartggw	sngcnttyws	ntgyttycar	240

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aaraarytna armgnaarcc nccnwsnacb aaygcnggnm gnmgnacraa rcaymgnytn	360
acntgyccnw sntgygayws ntaygaraar aarccnccna argarttyyt ngarmgntty	420
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aaatggaaat gaatatTTTT ccaattatta atccccaag tcattgaaaa taagcataac	180
cattctactg acttggttaga ctctaaacta acataaaaata cattttcaga aataaattca	240
accgatctta cctttacatc ttgtggagct gatagaagtt caggatccta agaaaattaa	300
ccaaagagta ttagttctga gttggtgata caagtcaaaa ggctcctttt gcattaatta	360
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<210> 7
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<213> Homo sapiens

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24

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204

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26

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 $\langle 220 \rangle$

16

25

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206

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His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu
35 40 45

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Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu
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His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn
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Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg
85 90 95

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Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala
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Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe
115 120 125

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Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu
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agtttttaatg	ttttgagtac	tcttacagga	acacctgacc	acacttttga	gttaaatttt	2641
atcccaagtg	tgatatttag	ttgttcaaaa	agggaaggga	tatacataca	tacatacata	2701
catacataca	tatatatata	tatatataca	tatatatata	tatatatatg	tatatatata	2761
tatatataga	gagagagaga	gagagagaga	gagaaagaga	gagaggttgt	tgtaggtcat	2821
aggagttcag	aggaaatcag	ttatggccgt	taatactgta	gctgaaagtg	ttttctttgt	2881
gaataaattc	atagcattat	tgatctatgt	tattgctctg	ttttattttac	agtcacacct	2941
gagaatttag	ttttaatatg	aatgatgtac	tttataactt	aatgattatt	tattatgtat	3001
ttggttttga	atgtttgtgt	tcatggcttc	ttatttaaga	cctgatcata	ttaaatgcta	3061
cccagtcgga	a					3072

<210> 56

<211> 146

<212> PRT

<213> mus musculus

<400> 56

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 20 25 30
 Arg His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp
 35 40 45
 Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
 50 55 60
 Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
 65 70 75 80
 Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
 85 90 95
 Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile
 100 105 110
 Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
 115 120 125
 Phe Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His
 130 135 140
 Leu Ser
 145

<210> 57

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22283

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34

<210> 58

<211> 31

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<213> Artificial Sequence

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<223> Oligonucleotide primer ZC22284

<400> 58

31

<400> 59

$\langle 400 \rangle$ 60

<400> 61

212

<400> 62

<211> 483

<213> homo sapiens

<400> 63

<211> 57

<213> Artificial Sequence

<223> Oligonucleotide primer ZC22052

<400> 64

<211> 57

<213> Artificial Sequence

<223> Oligonucleotide primer ZC22053

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<223> Oligonucleotide primer ZC23116

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<211>. 35

<213> Artificial Sequence

<223> Oligonucleotide primer ZC20892

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35

<211> 32

<213> Artificial Sequence

<223> Oligonucleotide primer ZC20893

cgtatcggcg cgccttaca tggatggggtc tt

32

<211> 39

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22054

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39

<210> 71

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22055

<400> 71

tgcagtttaa actcaggaat cttcacttcc gt

32

<210> 72

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Huza1pha11L-1 peptide

<400> 72

Gln	Asp	Arg	His	Met	Ile	Arg	Met	Arg	Gln	Leu	Ile	Asp	Ile	Val	Asp
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Gln	Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	Phe	Leu	Pro	Ala
			20					25					30		
Pro	Glu	Asp	Val	Glu	Thr	Asn	Cys								
		35					40								

<210> 73

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Huza1pha11L-3 peptide

<400> 73

Cys	Pro	Ser	Cys	Asp	Ser	Tyr	Glu	Lys	Lys	Pro	Pro	Lys	Glu	Phe	Leu
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Glu Arg Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser
 20 25 30

<210> 74
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<400> 74
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<210> 75
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<220>
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<400> 75
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<210> 76
 <211> 17
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC447

<400> 76
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<210> 77
 <211> 18
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC976

<400> 77

<400> 81
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<210> 82
<211> 60
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<220>
<223> Oligonucleotide primer ZC19352

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<210> 83
<211> 42
<212> DNA
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<220>
<223> Oligonucleotide primer ZC19371

<400> 83
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<210> 84
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<212> DNA
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<220>
<221> CDS
<222> (1)...(1560)

<223> MBP-human zalpha11 Ligand fusion polynucleotide

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1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

219

220

ccg	cgt	gga	tcc	caa	gat	cgc	cac	atg	att	aga	atg	cgt	caa	ctt	ata	1200
Pro	Arg	Gly	Ser	Gln	Asp	Arg	His	Met	Ile	Arg	Met	Arg	Gln	Leu	Ile	
385					390					395					400	
gat	att	gtt	gat	cag	ctg	aaa	aat	tat	gtg	aat	gac	ttg	gtc	cct	gaa	1248
Asp	Ile	Val	Asp	Gln	Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	
				405					410						415	
ttt	ctg	cca	gct	cca	gaa	gat	gta	gag	aca	aac	tgt	gag	tgg	tca	gct	1296
Phe	Leu	Pro	Ala	Pro	Glu	Asp	Val	Glu	Thr	Asn	Cys	Glu	Trp	Ser	Ala	
			420					425							430	
ttt	tcc	tgt	ttt	cag	aag	gcc	caa	cta	aag	tca	gca	aat	aca	gga	aac	1344
Phe	Ser	Cys	Phe	Gln	Lys	Ala	Gln	Leu	Lys	Ser	Ala	Asn	Thr	Gly	Asn	
		435					440					445				
aat	gaa	agg	ata	atc	aat	gta	tca	att	aaa	aag	ctg	aag	agg	aaa	cca	1392
Asn	Glu	Arg	Ile	Ile	Asn	Val	Ser	Ile	Lys	Lys	Leu	Lys	Arg	Lys	Pro	
	450					455					460					
cct	tcc	aca	aat	gca	ggg	aga	aga	cag	aaa	cac	aga	cta	aca	tgc	cct	1440
Pro	Ser	Thr	Asn	Ala	Gly	Arg	Arg	Gln	Lys	His	Arg	Leu	Thr	Cys	Pro	
465					470					475					480	
tca	tgt	gat	tct	tat	gag	aaa	aaa	cca	ccc	aaa	gaa	ttc	cta	gaa	aga	1488
Ser	Cys	Asp	Ser	Tyr	Glu	Lys	Lys	Pro	Pro	Lys	Glu	Phe	Leu	Glu	Arg	
				485					490						495	
ttc	aaa	tca	ctt	ctc	caa	aag	atg	att	cat	cag	cat	ctg	tcc	tct	aga	1536
Phe	Lys	Ser	Leu	Leu	Gln	Lys	Met	Ile	His	Gln	His	Leu	Ser	Ser	Arg	
			500					505							510	
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Thr	His	Gly	Ser	Glu	Asp	Ser	*									
		515														

<210> 85

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-human zalpha11 Ligand fusion polypeptide

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			20					25					30		
Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe
		35					40					45			
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala
	50					55					60				
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile
65				70						75					80
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp
				85					90					95	
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu
			100					105					110		
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys
		115					120					125			
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly
	130					135					140				
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro
145				150					155						160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys
				165					170					175	
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly
		180						185					190		
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp
		195					200					205			
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala
	210					215					220				
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys
225					230					235					240
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser
				245					250					255	
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro
			260					265					270		
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp
		275					280					285			
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala
	290					295					300				
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala
305					310					315					320
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln
				325					330					335	
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala
			340					345					350		

Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
 385 390 395 400
 Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
 405 410 415
 Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
 420 425 430
 Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
 435 440 445
 Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
 450 455 460
 Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
 465 470 475 480
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
 485 490 495
 Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
 500 505 510
 Thr His Gly Ser Glu Asp Ser
 515

<210> 86
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC22849

<400> 86
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 actt 64

<210> 87
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<220>
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<400> 87
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64

<213> Artificial Sequence

<223> MBP-mouse za1pha11 Ligand fusion polynucleotide

 $\langle 222 \rangle \quad (1) \dots (1533)$

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Met	Lys	Thr	Glu	Glu	Gly	Lys	Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	
1				5					10					15		

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc 144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca 192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc 240
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat 288
Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa 336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa 384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

acc	tgg	gaa	gag	atc	ccg	gcg	ctg	gat	aaa	gaa	ctg	aaa	gcg	aaa	ggt	432
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
	130					135					140					
aag	agc	gcg	ctg	atg	ttc	aac	ctg	caa	gaa	ccg	tac	ttc	acc	tgg	ccg	480
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	
145					150					155					160	
ctg	att	gct	gct	gac	ggg	ggt	tat	gcg	ttc	aag	tat	gaa	aac	ggc	aag	528
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	
				165				170						175		
tac	gac	att	aaa	gac	gtg	ggc	gtg	gat	aac	gct	ggc	gcg	aaa	gcg	ggt	576
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	
			180					185					190			
ctg	acc	ttc	ctg	gtt	gac	ctg	att	aaa	aac	aaa	cac	atg	aat	gca	gac	624
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	
		195					200					205				
acc	gat	tac	tcc	atc	gca	gaa	gct	gcc	ttt	aat	aaa	ggc	gaa	aca	gcg	672
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	
	210					215					220					
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Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	
225					230					235					240	
gtg	aat	tat	ggt	gta	acg	gta	ctg	ccg	acc	ttc	aag	ggt	caa	cca	tcc	768
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	
			245					250						255		
aaa	ccg	ttc	gtt	ggc	gtg	ctg	agc	gca	ggt	att	aac	gcc	gcc	agt	ccg	816
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	
			260					265					270			
aac	aaa	gag	ctg	gca	aaa	gag	ttc	ctc	gaa	aac	tat	ctg	ctg	act	gat	864
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	
		275				280						285				
gaa	ggt	ctg	gaa	gcg	gtt	aat	aaa	gac	aaa	ccg	ctg	ggt	gcc	gta	gcg	912
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	
	290					295					300					

226

tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc cta gaa aga 1488
 Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg
 485 490 495

cta aaa tgg ctc ctt caa aag atg att cat cag cat ctc tcc tga 1533
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<210> 89

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-mouse zalpha11 Ligand fusion polypeptide

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Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	35		40		45		
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	50		55		60		
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	65		70		75		80
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	85		90		95		
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	100		105		110		
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	115		120		125		
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	130		135		140		
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	145		150		155		160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	165		170		175		
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	180		185		190		
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	195		200		205		

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<210> 90
<211> 22
<212> DNA
<213> Artificial Sequence
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228

22

23

31

20

229

<400> 94
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<210> 95
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Human zalpha11 TaqMan probe. ZG31

<400> 95
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<210> 96
<211> 1821
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(1821)
<223> MBP-zalpha11 soluble receptor polynucleotide
sequence

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1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc 144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca 192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

231

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Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	
			245						250					255		
aaa	ccg	ttc	gtt	ggc	gtg	ctg	agc	gca	ggt	att	aac	gcc	gcc	agt	ccg	816
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	
			260					265					270			
aac	aaa	gag	ctg	gca	aaa	gag	ttc	ctc	gaa	aac	tat	ctg	ctg	act	gat	864
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	
		275					280					285				
gaa	ggt	ctg	gaa	gcg	gtt	aat	aaa	gac	aaa	ccg	ctg	ggt	gcc	gta	gcg	912
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	
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Gly	Ile	Lys 35	Val	Thr	Val	Glu	His 40	Pro	Asp	Lys	Leu	Glu 45	Glu	Lys	Phe
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His 65	Asp	Arg	Phe	Gly	Gly 70	Tyr	Ala	Gln	Ser	Gly 75	Leu	Leu	Ala	Glu	Ile 80
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Ala	Val	Arg	Tyr 100	Asn	Gly	Lys	Leu	Ile 105	Ala	Tyr	Pro	Ile	Ala 110	Val	Glu
Ala	Leu	Ser 115	Leu	Ile	Tyr	Asn 120	Lys	Asp	Leu	Leu	Pro	Asn 125	Pro	Pro	Lys
Thr	Trp 130	Glu	Glu	Ile	Pro	Ala 135	Leu	Asp	Lys	Glu	Leu 140	Lys	Ala	Lys	Gly
Lys 145	Ser	Ala	Leu	Met	Phe 150	Asn	Leu	Gln	Glu	Pro	Tyr 155	Phe	Thr	Trp	Pro 160
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Tyr	Asp	Ile	Lys 180	Asp	Val	Gly	Val	Asp 185	Asn	Ala	Gly	Ala	Lys 190	Ala	Gly
Leu	Thr	Phe 195	Leu	Val	Asp	Leu	Ile 200	Lys	Asn	Lys	His	Met 205	Asn	Ala	Asp
Thr	Asp 210	Tyr	Ser	Ile	Ala	Glu 215	Ala	Ala	Phe	Asn	Lys 220	Gly	Glu	Thr	Ala
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234

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Lys	Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly
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Thr	Glu 50	Leu	Thr	Val	Thr	Asp 55	Ile	Phe	Ala	Ala	Ser 60	Lys	Asn	Thr	Thr
Glu 65	Lys	Glu	Thr	Phe	Cys 70	Arg	Ala	Ala	Thr	Val 75	Leu	Arg	Gln	Phe	Tyr 80
Ser	His	His	Glu	Lys 85	Asp	Thr	Arg	Cys	Leu 90	Gly	Ala	Thr	Ala	Gln 95	Gln
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<213> Homo sapiens

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Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys
65					70					75					80
Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met
				85				90						95	
Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser
			100					105					110		

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<211> 538
<212> PRT
<213> Homo sapiens
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243

Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 275 280 285
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 290 295 300
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 305 310 315 320
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 465 470 475 480
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 485 490 495
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
 500 505 510
 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro
 515 520 525
 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
 530 535